

Hongding Gao | Curriculum Vitae

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Born: 19. October, 1984

Fields of Interest

- Statistical models in quantitative genetics and genomics
- New phenotypes and high-throughput phenotyping in animal breeding
- Software development in genetic and genomic evaluation

Education Background

- Ph.D. Dept. of Animal Science and Technology, China Agricultural University, P.R.China, 2007 - 2012
- Ph.D. Center for Quantitative Genetics and Genomics, Dept. of Molecular Biology and Genetics, Aarhus University, Denmark, 2009 - 2012
- B.Sc. Dept. of Animal Science and Technology, China Agricultural University, P.R.China, 2002 - 2006

Professional Experience

- Researcher/Assistant Professor, Center for Quantitative Genetics and Genomics, Dept. of Molecular Biology and Genetics, Aarhus University, Denmark, 2018 -
- Postdoc, Center for Quantitative Genetics and Genomics, Dept. of Molecular Biology and Genetics, Aarhus University, Denmark, 2013 - 2017
- Industrial Postdoc program, Breakthrough Leadership Program, Harvard Business School, Apr. 2015 - Jan. 2016
- Visiting scientist, AGBU, University of New England, Australia, Feb. 2020 - Apr. 2020
- Visiting scientist, Dept. of Animal Science, Iowa State University, U.S. Dec. 2015 - Feb. 2016
- Visiting scientist, Natural Resources Institute Finland (Luke), Finland, Nov. 2016 - Jan. 2017
- Director, Dairy Cattle Genetic Evaluation, Dairy Association of China, Beijing, P.R.China, 2012 - 2013

Research Grants

- Danish National Advanced Technology Foundation no.140-2013-6, 2014 - 2017

Teaching and Supervision

- Co-supervising Ph.D. student Farzad Afiani, 2019, with Just Jensen
- Course "Linear Models" at Copenhagen University (Master students) 2018, with Ole F. Christensen

Software

- o ssBr: A software toolbox for genomic prediction and variance component estimation based on single-step model using Bayesian methods for large-scale data (Fortran 90). Software has been developed for parallel computing

Publications

- o **Gao H.**, G. Su, P. Madsen, O. F. Christensen, J. Jensen, B. Ask, B. G. Poulsen, T. Ostensen and B. Nielsen. 2020. Joint analysis of group- and individual-level feed intake records using a bivariate random regression single-step model in pigs. *Genetics Selection Evolution* (under review)
- o Li J., **Gao H.***, P. Madsen, W. Liu, P. Bao, G. Xue, Y. Gao, X. Di and G. Su. 2020. Impact of the order of Legendre polynomials in random regression model on genetic evaluation for milk yield in dairy cattle population. *Frontiers in Genetics* (*co-first author)
- o Berg. P., **H. Gao**, J. R. Thomasen, A. C. Sørensen, Line Hjortø. 2020. Definition of relationship matrix used in optimal-contribution selection impacts genetic diversity maintained. *Genetics Selection Evolution* (under review)
- o Milkevych V., P. Madsen, **H. Gao**, J. Jensen. 2020. The relative effect of genomic information on efficiency of Bayesian analysis of the mixed linear model with unknown variance. *Journal of Animal Breeding and Genetics*
- o Ma X., O. F. Christensen, **H. Gao**, R. Huang, B. Nielsen, P. Madsen, J. Jensen, T. Ostensen, P. Li, M. Shirali, G. Su. 2020. Prediction of breeding values for group recorded traits including genomic information and an individually recorded correlated trait. *Heredity*
- o **Gao H.**, P. Madsen, G. P. Aamand, J. R. Thomasen, A. C. Sørensen and J. Jensen. 2019 Effects of genomic selection on estimation of variance components: a simulation study. *BMC Genomics*
- o **Gao H.**, B. Nielsen, G. Su, P. Madsen, J. Jensen, O. F. Christensen, T. Ostensen and M. Shirali. 2019 Use of repeated group measurements with drop out animals for variance component estimation and genetic prediction. *G3: GENES, GENOMES, GENETICS*
- o Zhang T., **Gao H.**, S. Goutam, H. Fan, . . . , F. Zhao. 2019. Genome-wide association studies reveal candidate genes for fat deposition in tails and body size in Hulun Buir sheep. *Journal of Animal Breeding and Genetics*
- o Fan H., Y. Hou, G. Sahana, **H. Gao**, C. Zhu, L. Du, L. Wang, and F. Zhao. 2019. The metabolism of tail fat in two types of Hulun Buir sheep according to tail size and sex. *Animals*
- o **Gao H.**, M. Koivula, I. Strandén, J. Jensen, P. Madsen, T. Pitkänen, G. P. Aamand, and Mäntysaari E. 2018. Short communication: Genomic prediction using different single-step methods in the Finnish red dairy cattle population. *Journal of Dairy Science*

- o **Gao H.**, P. Madsen, J. Pösö, G. P. Aamand, M. Lidauer and J. Jensen. 2018. Short communication: Multivariate outlier detection for routine Nordic dairy cattle genetic evaluation in the Nordic Holstein and Red population. *Journal of Dairy Science*
- o Zhang Z., Q. Zhang, . . . , **H. Gao**, . . . , Y. Pan. 2018. The distribution of runs of homozygosity in Chinese and western pig breeds evaluated by reduced-representation sequencing data. *Animal Genetics*
- o Wang, X., **H. Gao**, K. G. Gebremedhin, B. S. Bjerg, J. Van Os, C. B. Tucker, and G. Zhang. 2018. A Predictive Model of Equivalent Temperature Index for Dairy Cattle (ETIC). *Journal of Thermal Biology* 76:165-170
- o Ma, P., J. Huang, W. Gong, X. Li, **H. Gao**, Q. Zhang, X. Ding and C. Wang. 2018. The impact of genomic relatedness between populations on the genomic estimated breeding values. *Journal of Animal Science and Biotechnology* 9:64
- o **Gao, H.**, P. Madsen, U. S. Nielsen, G. P. Aamand, G. Su, K. Byskov, and J. Jensen. 2015. Including different groups of genotyped females for genomic prediction in a Nordic Jersey population. *Journal of Dairy Science* 98(12):9051-9059
- o **Gao, H.**, G. Su, L. Janss, Y. Zhang, and M. S. Lund. 2013. Model comparison on genomic predictions using high-density markers for different groups of bulls in the Nordic Holstein population. *Journal of Dairy Science* 96(7):4678-4687
- o **Gao, H.**, M. Lund, Y. Zhang, and G. Su. 2013. Accuracy of genomic prediction using different models and response variables in the Nordic Red cattle population. *Journal of Animal Breeding and Genetics*
- o **Gao, H.**, O. F. Christensen, P. Madsen, U. S. Nielsen, Y. Zhang, M. S. Lund, and G. Su. 2012. Comparison on genomic predictions using three GBLUP methods and two single-step blending methods in the Nordic Holstein population. *Genetics Selection Evolution* 44:8